AMENDMENTS TO THE CLAIMS

This listing of the claims will replace all prior versions, and listings, of claims in the application.

1. (currently amended) A method for characterizing a SAGE tag fragment comprising:

a) obtaining a RNA sample from the same tissue type as used in generating said SAGE tag;

b) generating a cDNA fragment comprising the sequence of the SAGE tag from said RNA sample by performing a DNA amplification reaction wherein primers used comprise:

(i) a SAGE tag sequence as a sense primer; and

(ii) at least one single-base anchored oligo-dT primer as an antisense primer; and

c) analyzing said cDNA fragments.

2. (original) The method of claim 1, wherein said RNA sample is the RNA sample used to perform SAGE.

3. (previously presented) The method of claim 1, wherein said DNA amplification comprises a polymerase chain reaction.

4. (original) The method of claim 3, wherein the DNA polymerase used for said polymerase chain reaction is *Pfu* DNA polymerase.

5. (previously presented) The method of claim 3, comprising a Mg^{2+} concentration of 4 mM.

6. (previously presented) The method of claim 1, wherein said cDNA fragment generated is about 50 to 600 base pairs in length.

7. (currently amended) The method of claim 1, wherein said single-base anchored oligo-dT primer comprises a single-base anchored to the 3' end of the oligo-dT primer, said single base excluding dT.

8. (currently amended) The method of claim 1, wherein said single-base anchored oligo-dT primer comprises from 10 to 25 poly-dT residues.

9. (currently amended) The method of claim 8, wherein said single-base anchored oligo-dT primer comprises 11 poly-dT residues.

10. (original) The method of claim 1, wherein said sense primer further comprises a *Bam*HI recognition sequence at the 5' end.

11. (original) The method of claim 1, wherein said SAGE tag further comprises a *Nla*III recognition sequence at the 5' end.

12. (previously presented) The method of claim 1, wherein said analyzing comprises:

i) cloning said cDNA fragment; and

ii) sequencing said clone to identify said cDNA fragment sequence.

13. (previously presented) The method of claim 12, further comprising comparing the cDNA sequence to known sequences.

14. (previously presented) The method of claim 1, wherein said analyzing comprises hybridizing the cDNA fragments with a known sequence.

15. (previously presented) The method of claim 1, wherein said analyzing comprises cloning a full-length cDNA.

16. (previously presented) The method of claim 1, wherein said analyzing comprises performing a DNA amplification reaction comprising:

i) a sense primer designed based on an existing exon sequence; and

ii) a single-base anchored oligo-dT primer as an antisense primer, thereby generating an amplified DNA; and further comprising

iii) cloning and sequencing the amplified DNA.

17. (previously presented) The method of claim 16, wherein the exon sequences are predicted by a bioinformatics tool.

18. (previously presented) The method of claim 17, further comprising aligning the sequence of the amplified cDNA with a genomic DNA sequence.

19. (original) The method of claim 1, wherein the tissue type is selected from the group consisting of colon, thymus, small intestine, heart, placenta, skeletal muscle, testes, bone marrow, trachea, spinal cord, liver, spleen, brain, lung, ovary, prostate, skin, cornea, retina, and breast.

20. (original) The method of claim 15, wherein the full length cDNA is cloned into an expression vector.

21-41. (Canceled)